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On page 1, line 10, change "07/267,865" to --07/267,685--.

On page 18, line 18, change "vestors" (both occurrences) to --vectors--.

On page 21, line 11, change "monocatoledenous" to --monocotyledenous--.

On page 21, line 18, change "10<sub>8</sub>" to --10<sup>8</sup>--.

On page 28, lines 9-10, change "12301 Parklawn Drive, Rockville, Maryland, 20852"

C' to --10801 University Blvd., Manassas, VA 20110--.

On page 30, line 25, change "<sup>32</sup>p" to --<sup>32</sup>P--.

On page 30, line 26, change "amioglycoside" to --aminoglycoside--.

On page 31, line 5, change "ianamycin" to --kanamycin--.

On page 31, line 7, change "(1984) \_\_\_\_ : \_\_\_\_" to --(1985) 4(1):25-32--.

On page 31, line 13, change "1.1kd" to --1.1kb--.

On page 32, lines 4 and 7, change "1.0kb" to --1.0kb--.

On page 38, line 8, change "eas" to --ease--.

On page 58, lines 19, 23 and 32, change "PCGN" to --pCGN--.

On page 59, line 15, change "MRNA" to --mRNA--.

On page 65, lines 7 and 23, change "<sup>32</sup>p" to --<sup>32</sup>P--.

On page 65, line 11, change "toot" to --root--.

On page 67, line 9, change "<sup>32</sup>p" to --<sup>32</sup>P--.

On page 74, line 12, change "SAcI" to --SacI--.

On page 75, lines 26 and 27, change "XHOI" to --Xhol--.

IN THE CLAIMS:

C2 17. (Twice Amended) A method for obtaining a plant which produces at least one seed having a modified phenotype, said method comprising:

transforming a host plant cell with a DNA construct under genomic integration conditions, wherein said construct comprises as operably linked components in the direction of transcription, a promoter region obtainable from a gene, wherein transcription of said gene is preferentially regulated in plant seed tissue, a DNA sequence of interest other than the native

coding sequence of said gene, and a transcription termination region, wherein said components are functional in a plant cell,

whereby said DNA construct becomes integrated into a genome of said plant cell, regenerating a plant from said transformed plant cell, and growing said plant under conditions whereby said DNA sequence of interest is expressed and a [plant] seed having said modified phenotype is obtained.

*C2*  
18. (Twice Amended) A method of altering the phenotype of plant seed tissue as distinct from other plant tissue, said method comprising:

growing a plant which produces at least one seed, wherein said plant comprises cells containing a DNA construct integrated into their genome, said DNA construct comprising, in the 5' to 3' direction of transcription, a transcriptional initiation region from a gene, wherein transcription of said gene is preferentially regulated in a plant seed tissue, a DNA sequence of interest other than the coding sequence native to said transcriptional initiation region, and a transcriptional termination region, whereby transcription of said DNA sequence of interest is [transcribed under transcriptional control of] controlled by said transcriptional initiation region and [a] plant seed tissue having an altered phenotype is obtained.

19. (Reiterated) The method according to Claim 17 or 18, wherein said DNA construct is flanked by T-DNA.

*C3*  
20. (Amended) The method according to Claim 19, wherein said plant is selected from the group consisting of soybean, [or] rapeseed [plant] and tomato.

21. (Reiterated) The method according to Claim 17 or 18 wherein said DNA sequence of interest encodes an enzyme.

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22. (Reiterated) The method according to Claim 17 or 18 wherein said DNA sequence of interest is an antisense sequence.

23. (Amended) [The] A method [according to Claim 17 or 18] for obtaining a plant which produces at least one seed having a modified phenotype, said method comprising:

*C4*  
transforming a host plant cell with a DNA construct under genomic integration conditions, wherein said construct comprises as operably linked components in the direction of transcription, a promoter region obtainable from a gene, wherein said gene is preferentially transcribed during seed embryogenesis, a DNA sequence of interest other than the native coding sequence of said gene, and a transcription termination region, wherein said components are functional in a plant cell,

*Sub E2*  
whereby said DNA construct becomes integrated into a genome of said plant cell, regenerating a plant from said transformed plant cell, and growing said plant under conditions whereby said DNA sequence of interest is expressed and a plant having said seed with a modified phenotype is obtained.

*17* *15 16*  
24. (Amended) The method according to Claim 23 or 52, wherein said gene is transcribed from about day 7 to day 40 postanthesis.

*C5* *8*  
25. (Reiterated) The method according to Claim 17 or 18 wherein said gene is transcribed during seed maturation.

*7*  
26. (Amended) The method according to Claim 25 wherein said gene is transcribed from about day 11 to day 30 postanthesis.

27. (Reiterated) The method according to Claim 18, wherein said transcriptional initiation region further comprises a translational initiation region and said DNA sequence of interest is an open reading frame encoding an amino acid sequence.

28. (Amended) A method for modifying a genotype of a plant to impart a desired characteristic to seed as distinct from other plant tissue, said method comprising:  
C6  
transforming under genomic integration conditions, a host plant cell with a DNA construct comprising in the 5' to 3' direction of transcription, a transcriptional initiation region from a gene, wherein [said] transcription of said gene is preferentially regulated in a plant seed tissue, a DNA sequence of interest other than the native coding sequence of said gene, and a transcriptional termination region, whereby said DNA construct becomes integrated into the genome of said plant cell;  
regenerating a plant from said transformed host cell; and  
growing said plant to produce seed under conditions whereby said DNA sequence of interest is expressed and a plant having a modified genotype is obtained.

29. (Reiterated) The method according to Claim 28, wherein said DNA construct is flanked by T-DNA.

30. (Reiterated) The method according to Claim 28, wherein said plant is a *Brassica* plant.

31. (Reiterated) The method according to Claim 28, wherein said DNA sequence of interest encodes an enzyme.

32. (Reiterated) The method according to Claim 28, wherein said DNA sequence of interest is an antisense sequence.

18  
23  
33. (Amended) The method according to Claim 28, wherein said plant is a soybean or a tomato plant.

34. (Reiterated) A method for modifying transcription in seed tissue as distinct from other plant tissue, said method comprising:

growing a plant capable of developing seed tissue under conditions to produce seed, wherein said plant comprises cells containing a DNA construct integrated into their genome, said DNA construct comprising, in the 5' to 3' direction of transcription, a seed-specific transcriptional initiation region, a DNA sequence of interest other than the coding sequence native to said transcriptional initiation region, and a transcriptional termination region, whereby transcription of said DNA sequence of interest is [transcribed under transcriptional control of] controlled by said seed-specific transcriptional initiation region.

35. (Reiterated) The method according to Claim 34, wherein said DNA sequence of interest is an antisense sequence.

36. (Reiterated) The method according to Claim 34, wherein said plant is of the genus *Brassica*.

37. (Reiterated) The method according to Claim 34, wherein said transcriptional initiation region further comprises a translational initiation region and said DNA sequence of interest is an open reading frame encoding an amino acid sequence.

*C 8* *28*  
38. (Amended) The method according to Claim 34, wherein said plant is a soybean or a tomato plant.

39. (Reiterated) A method to selectively express a heterologous DNA sequence of interest in seed tissue as distinct from other plant tissue, said method comprising:

growing a plant capable of developing a seed tissue under conditions to produce seed, wherein said plant comprises cells having a genomically integrated DNA construct comprising, as operably linked components in the 5' to 3' direction of transcription, a seed-specific

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transcriptional initiation region and a translational initiation region, a DNA sequence of interest other than the coding sequence native to said transcriptional initiation region, a transcriptional termination region downstream of said DNA sequence of interest, whereby said DNA sequence of interest is expressed under control of said seed-specific transcriptional and translational initiation region.

40. (Reiterated) The method according to Claim 39, wherein said plant is of the genus *Brassica*.

<sup>31</sup> <sup>29</sup> 41. (Amended) The method according to Claim <sup>39</sup>, wherein said plant is a soybean or a tomato plant.

<sup>35</sup> 42. (Amended) A method [according to Claim 17 or Claim 18] for obtaining a plant which produces at least one seed having a modified phenotype, said method comprising:

<sup>19</sup> transforming a host plant cell with a DNA construct under genomic integration conditions, wherein said construct comprises as operably linked components in the direction of transcription, a promoter region obtainable from a gene, wherein transcription of said gene is preferentially regulated in plant seed tissue and said gene is selected from the group consisting of a napin gene, an ACP gene, [cruciferin gene, or] and an EA9 gene, a DNA sequence of interest other than the native coding sequence of said gene, and a transcription termination region, wherein said components are functional in a plant cell,

whereby said DNA construct becomes integrated into a genome of said plant cell, regenerating a plant from said transformed plant cell, and  
growing said plant under conditions whereby said DNA sequence of interest is expressed and a plant having said seed with a modified phenotype is obtained.

43. (Reiterated) The method according to Claim 17 or Claim 18, wherein said DNA sequence of interest is a structural gene.

44. (Reiterated) The method according to Claim 17 or Claim 18, wherein said DNA sequence of interest is an open reading frame encoding an amino acid sequence.

45. (Reiterated) The method according to Claim 17 or Claim 18; wherein said transcriptional initiation region further comprises a translational initiation region.

46. (Amended) A method for modifying transcription in plant seed tissue as distinct from other plant tissue, said method comprising:

growing a plant wherein said plant comprises cells containing a DNA construct integrated into their genome, said construct comprising:

a regulatory transcriptional initiation region from a gene wherein said gene is preferentially expressed in plant seed tissue; a DNA sequence of interest other than the coding sequence native to said regulatory regions, whereby expression of transcriptional initiation region, wherein said DNA sequence of interest is controlled by said regulatory regions transcriptional initiation region, whereby transcription in said plant seed tissue is modified as distinct from other plant tissue.

33 32  
47. (Amended) The method according to Claim 46, wherein said regulatory region comprise transcriptional and] DNA construct further comprises a translational initiation region and a termination region[s].

48. (Amended) A method to selectively express a heterologous DNA sequence of interest in plant seed tissue as distinct from other plant tissue, said method comprising: growing a plant wherein said plant comprises cells containing a DNA construct integrated into their genome, said construct comprising as operably linked components in the direction of transcription a promoter region from a gene preferentially expressed in plant seed tissue specific expression cassette] and a DNA sequence of interest, wherein said DNA sequence of

*C 110*  
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*Sub E 1*

interest is other than the coding sequence native to said promoter region and is expressed under the control of said [tissue specific expression cassette] promoter region whereby said DNA sequence of interest is expressed in plant seed tissue.

Please add the following new claims:

*111*  
--49. (New) A method according to Claim 17 or Claim 18, wherein said gene is a cruciferin gene. *1*

*112*  
50. (New) A method according to Claim 17, wherein said promoter region is from a gene encoding a storage protein. *2*

*113*  
51. (New) A method according to Claim 18, wherein said transcriptional initiation region is from a gene encoding a storage protein. *2*

*114*  
52. (New) A method of altering the phenotype of plant seed tissue as distinct from other plant tissue, said method comprising:

*115*  
growing a plant, wherein said plant comprises cells containing a DNA construct integrated into their genome, said DNA construct comprising, in the 5' to 3' direction of transcription, a transcriptional initiation region from a gene, wherein said gene is preferentially transcribed during seed embryogenesis, a DNA sequence of interest other than the coding sequence native to said transcriptional initiation region, and a transcriptional termination region, whereby transcription of said DNA sequence of interest is controlled by said transcriptional initiation region and plant seed tissue having an altered phenotype is obtained.

*116*  
53. (New) A method of altering the phenotype of plant seed tissue as distinct from other plant tissue, said method comprising:

growing a plant, wherein said plant comprises cells containing a DNA construct integrated into their genome, said DNA construct comprising, in the 5' to 3' direction of transcription, a transcriptional initiation region from a gene, wherein transcription of said gene is preferentially regulated in plant seed tissue and said gene is selected from the group consisting of a napin gene, an ACP gene and an EA9 gene, a DNA sequence of interest other than the coding sequence native to said transcriptional initiation region, and a transcriptional termination region, whereby transcription of said DNA sequence of interest is controlled by said transcriptional initiation region and plant seed tissue having an altered phenotype is obtained.

*011* 37 35 36  
54. (New) The method according to Claim ~~42~~ or ~~53~~, wherein said plant is a dicotyledonous plant.

*38* 37  
55. (New) The method according to Claim ~~54~~, wherein said dicotyledonous plant is selected from the group consisting of rapeseed, soybean, safflower, sunflower and tomato.

*39* 35 36  
56. (New) The method according to Claim ~~42~~ or ~~53~~, wherein said DNA construct further comprises a translational initiation region.

*40* 35 36  
57. (New) The method according to Claim ~~42~~ or ~~53~~, wherein said DNA construct is flanked by T-DNA.

*41* 35 36  
58. (New) The method according to Claim ~~42~~ or ~~53~~, wherein said DNA sequence of interest comprises an open reading frame encoding an amino acid sequence.

*42* 35 36  
59. (New) The method according to Claim ~~42~~ or ~~53~~, wherein said DNA sequence of interest encodes an enzyme.

43 60. (New) The method according to Claim 42 or 53, wherein said DNA sequence of interest is complementary to an mRNA endogenous to a plant cell.

61. (New) A method for obtaining a plant which produces at least one seed having a modified phenotype, said method comprising:

transforming a host plant cell with a DNA construct under genomic integration conditions, wherein said construct comprises as operably linked components in the direction of transcription, a promoter region obtainable from a gene encoding a seed storage protein, wherein transcription of said gene is preferentially regulated in plant seed tissue, a DNA sequence of interest other than the native coding sequence of said gene, and a transcription termination region, wherein said components are functional in a plant cell,

whereby said DNA construct becomes integrated into a genome of said plant cell,

regenerating a plant from said transformed plant cell, and

growing said plant under conditions whereby said DNA sequence of interest is expressed and a plant having said seed with a modified phenotype is obtained.

*Sub E10*  
62. (New) A method of altering the phenotype of plant seed tissue as distinct from other plant tissue, said method comprising:

growing a plant, wherein said plant comprises cells containing a DNA construct integrated into their genome, said DNA construct comprising, in the 5' to 3' direction of transcription, a transcriptional initiation region from a gene encoding a seed storage protein, wherein transcription of said gene is preferentially regulated in a plant seed tissue, a DNA sequence of interest other than the coding sequence native to said transcriptional initiation region, and a transcriptional termination region, whereby transcription of said DNA sequence of interest is controlled by said transcriptional initiation region and plant seed tissue having an altered phenotype is obtained.--.